

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2004, 11:35:32 ; Search time 9.10345 Seconds

(without alignments)  
84.532 Million cell updates/sec

Title: SEQ3  
Perfect score: 43

Sequence: 1 qppraaly 8

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 75 summaries

Database :

PIR\_78:\*  
1: pirl:\*  
2: pirl:\*  
3: pirl:\*  
4: pirl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Score	Match Length	ID	Description
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No matches found

Search completed: July 28, 2004, 11:59:05  
Job time : 9.10345 secs

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OM protein - protein search, using sw model

Run on: July 28, 2004, 11:34:37 ; Search time 5.10345 Seconds

(without alignments)  
81.623 Million cell updates/sec

Title: SEQ3

Perfect score: 43

Sequence: 1 qppraaiy 8

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 75 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query		
No.	Score	Match Length	ID
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Description			
-----			

No matches found

Search completed: July 28, 2004, 11:49:10  
Job time : 5.10345 secs

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## OM protein - protein search, using sw model

Run on: July 28, 2004, 11:35:02 ; Search time 30.4828 Seconds

(Without alignments)  
82.806 Million cell updates/sec

Title: SEQ3

Perfect score: 43

Sequence: 1 qppraaly 8

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 75 summaries

Database :

SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description
-----		
No matches found		

Search completed: July 28, 2004, 11:56:43  
Job time : 30.4828 secs

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OM protein - protein search, using sw model

Run on: July 28, 2004, 11:33:47 ; Search time 46.1379 Seconds

(without alignments)  
48.992 Million cell updates/sec

Title: SEQ3

Perfect score: 43  
Sequence: 1 qppraaly 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 75 summaries

Database: A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*\n2: geneseqp1990s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	8	AAAB19055	Aab19055 Amino aci
2	43	100.0	9	AAAY28517	Aay28517 Beta-1 in

#### ALIGNMENTS

#### RESULT 1

AAAB19055 standard; peptide; 8 AA.

08-FEB-2001 (first entry)

Amino acid sequence of a betal-integrin inhibitor.

Betal-integrin inhibitor; leukocyte mediated tissue destruction;

central nervous system ischemic injury; myocardial infarction;

betal-integrin; angioplasty; surgical incision; injury-related trauma;

transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.

Synthetic.

WO200056350-A2.

XX 28-SEP-2000.

XX 22-MAR-2000; 2000WO-US007680.

XX 22-MAR-1999; 99US-0125634P.

XX 24-NOV-1999; 99US-0167538P.

XX (MINT ) UNIV MINNESOTA.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (SENT-) SENTRON MEDICAL INC.

XX McCarthy JB, Milecki WJ, Jamieson GA, Low WC, Sawchuk RJ;

XX Furcht LT;

XX WPI; 2000-656062/63.

XX Inhibition of inflammatory leukocyte mediated destruction of tissue in a

XX patient, comprises administering a peptide inhibitor of betal-integrin,

XX useful for treatment of e.g. cancer and osteoporosis.

XX Claim 3; Page 38; 61pp; English.

XX AAAB19054-67 represent betal-integrin inhibitors. The peptides inhibit  
XX betal-integrin which is responsible for leukocyte mediated tissue  
XX destruction. The peptides are useful for inhibiting inflammatory  
XX leukocyte mediated destruction of tissue which occurs as a result of  
XX central nervous system (CNS) ischemic injury, myocardial infarction,  
XX angioplasty, surgical incisions, injury-related trauma, and/or transplant  
XX reperfusion, exposure to heat, cold, light, electricity and/or chemicals.  
XX They are also useful for the treatment of stroke, a burn type injury,  
XX cancer, and osteoporosis

XX Sequence 8 AA;

Query Match 100.0%; Score 43; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPPRAALY 8  
DB 1 QPPRAALY 8

#### RESULT 2

AAAY28517 standard; peptide; 9 AA.

AAAY28517;

DT 19-OCT-1999 (first entry)

DE Beta-1 integrin cell adhesion modulator analogue #8.

KM Beta 1 integrin dependent cell adhesion; lipid motif; tumour;

XX C-terminal tyrosine tagged; cancer; fibronectin; melanoma.

XX Synthetic.

XX WO9937669-A1.

XX 29-UTL-1999.

XX 21-JAN-1999; 99WO-US001236.

XX 22-JAN-1998; 98US-0072119P.

XX 12-AUG-1998; 98US-0096211P.

XX 12-AUG-1998; 98US-0096212P.

XX (MINT ) UNIV MINNESOTA.

XX McCarthy JB, Furcht LT, Brienzo A;

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OM protein - protein search, using sw model

Run on: July 28, 2004, 11:56:53 ; Search time 38.8966 Seconds

(Without alignments)  
64.516 Million cell updates/sec

Title: SEQ3  
Perfect score: 43  
Sequence: 1 qppraaiy 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/prodata/1/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/prodata/1/pubppaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/1/pubppaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/prodata/1/pubppaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/prodata/1/pubppaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/prodata/1/pubppaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/prodata/1/pubppaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/prodata/1/pubppaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/prodata/1/pubppaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/prodata/1/pubppaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/prodata/1/pubppaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/prodata/1/pubppaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/prodata/1/pubppaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/prodata/1/pubppaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/prodata/1/pubppaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/prodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			
No.			
Score	Query Match	Length DB	ID
Description			
No matches found			

Search completed: July 28, 2004, 12:58:37  
Job time : 38.8966 secs

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OM protein - protein search, using sw model

Run on: July 28, 2004, 11:36:28 ; Search time 12.418 Seconds

(without alignments)  
33.270 Million cell updates/sec

Title: SEQ3  
Perfect score: 43  
Sequence: 1 qppraaly 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 75 summaries

Database : Issued\_Patents\_AA:\*

1:	/cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2:	/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3:	/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4:	/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5:	/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6:	/cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
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No matches found

Search completed: July 28, 2004, 12:02:17  
Job time : 12.4805 secs